

10498-00067.ST25
SEQUENCE LISTING

<110> Ayad, Nagi

Kirschner, Marc

<120> NOVEL CELL CYCLE GENES REQUIRED FOR MITOTIC ENTRY

<130> 10498-00067

<150> 60/459,788

<151> 2003-04-02

<160> 7

<170> PatentIn version 3.1

<210> 1

<211> 266

<212> PRT

<213> Mus musculus

<400> 1

Met Gly Ser Thr Gln Ser Val Ser Gly Thr Pro Ala Arg Pro Leu Pro
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Arg Asn Lys Gln Val Ala Arg Val Ala Asp Pro Arg Ser Pro Ser Ala
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Gly Ile Gln Arg Thr Pro Ile Gln Val Glu Ser Ser Pro Gln Pro Ser
35 40 45

Leu Pro Ala Glu Gln Leu Asn Gly Leu Lys Gln Ala Gln Asp Pro Asp
50 55 60

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Pro Arg Ser Pro Thr Leu Gly Ile Ala Arg Thr Pro Met Lys Ile Ser
65 70 75 80

Gly Pro Asp Pro Gln Cys Ser Leu Val Lys Glu Leu Ser Glu Val Leu
85 90 95

Glu Thr Glu Ala Ser Glu Ser Ile Ser Ser Pro Glu Leu Ala Leu Pro
100 105 110

Arg Glu Thr Pro Leu Phe Tyr Asp Leu Asp Leu Ser Ser Asp Pro Gln
115 120 125

Leu Ser Pro Glu Asp Gln Leu Leu Pro Trp Ser Gln Ala Glu Leu Asp
130 135 140

Pro Lys Gln Val Phe Thr Lys Glu Glu Ala Lys Gln Ser Ala Glu Thr
145 150 155 160

Ile Ala Ala Ser Gln Asn Ser Asp Lys Pro Ser Arg Asp Pro Glu Thr
165 170 175

Pro Gln Ser Ser Gly Ser Lys Arg Ser Arg Arg Lys Ala Asn Ser Lys
180 185 190

Val Leu Gly Arg Ser Pro Leu Thr Ile Leu Gln Asp Asp Asn Ser Pro
195 200 205

Gly Thr Leu Thr Leu Arg Gln Gly Lys Arg Pro Ser Ala Leu Ser Glu
210 215 220

Asn Val Lys Asp Leu Lys Glu Gly Val Val Leu Gly Thr Gly Arg Phe
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Leu Lys Ala Gly Gly Gly Ala Arg Glu Pro Asn Gln Asp His Asp Lys
245 250 255

Glu Asn Gln His Phe Ala Leu Leu Glu Ser
260 265

<210> 2

<211> 268

<212> PRT

<213> Homo sapiens

<400> 2

Met Gly Ser Ala Lys Ser Val Pro Val Thr Pro Ala Arg Pro Pro Pro
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His Asn Lys His Leu Ala Arg Val Ala Asp Pro Arg Ser Pro Ser Ala
 20 25 30

Gly Ile Leu Arg Thr Pro Ile Gln Val Glu Ser Ser Pro Gln Pro Gly
 35 40 45

Leu Pro Ala Gly Glu Gln Leu Glu Gly Leu Lys His Ala Gln Asp Ser
 50 55 60

Asp Pro Arg Ser Pro Thr Leu Gly Ile Ala Arg Thr Pro Met Lys Thr
 65 70 75 80

Ser Ser Gly Asp Pro Pro Ser Pro Leu Val Lys Gln Leu Ser Glu Val
 85 90 95

Phe Glu Thr Glu Asp Ser Lys Ser Asn Leu Pro Pro Glu Pro Val Leu
 100 105 110

Pro Pro Glu Ala Pro Leu Ser Ser Glu Leu Asp Leu Pro Leu Gly Thr
 115 120 125

Gln Leu Ser Val Glu Glu Gln Met Pro Pro Trp Asn Gln Thr Glu Phe
 130 135 140

Pro Ser Lys Gln Val Phe Ser Lys Glu Glu Ala Arg Gln Pro Thr Glu
 145 150 155 160

Thr Pro Val Ala Ser Gln Ser Ser Asp Lys Pro Ser Arg Asp Pro Glu
 165 170 175

Thr Pro Arg Ser Ser Gly Ser Met Arg Asn Arg Trp Lys Pro Asn Ser
 180 185 190

Ser Lys Val Leu Gly Arg Ser Pro Leu Thr Ile Leu Gln Asp Asp Asn
 195 200 205

Ser Pro Gly Thr Leu Thr Leu Arg Gln Gly Lys Arg Pro Ser Pro Leu

210

215

220

Ser Glu Asn Val Ser Glu Leu Lys Glu Gly Ala Ile Leu Gly Thr Gly
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Arg Leu Leu Lys Thr Gly Gly Arg Ala Trp Glu Gln Gly Gln Asp His
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Asp Lys Glu Asn Gln His Phe Pro Leu Val Glu Ser
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<210> 3

<211> 363

<212> PRT

<213> *Xenopus laevis*

<400> 3

Met Gly Ser Ala Glu Ser Lys Ala Gln Val Thr Pro Ser Arg Pro Leu
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Arg Asn His Leu Leu Ser Arg Val Asn Asp Pro Arg Ser Pro Thr Ser
 20 25 30

Gly Ile Pro Arg Thr Pro Ile Glu Val Gly Glu Ser Pro Arg Asn Thr
 35 40 45

Pro Gln Thr Val Lys Glu Glu Glu Glu Ile Pro Asp Ser Pro Glu
 50 55 60

Ile Phe Asp Pro Arg Ser Pro Thr Asn Gly Ile Thr Arg Thr Pro Leu
 65 70 75 80

Arg Pro Pro Ile His Ala Val Leu Asn Asn Leu Ala Lys Gln Leu Ser
 85 90 95

Glu Val Phe Val Ala Glu Asp Ser Ser Thr Glu Gly Gly Pro Leu Gly
 100 105 110

Phe Thr Gly Pro Glu Ala Thr Asn Leu Glu Arg Gln Val Val Glu Ser
 115 120 125

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Gln	Thr	Ala	Pro	Pro	Ala	Gly	Glu	His	Val	Asn	Asp	His	Glu	Val	Glu	130	135	140
Pro	Ser	Val	Glu	Lys	Ala	Glu	Thr	Gln	Ile	Asp	Leu	Glu	Val	Cys	Pro	145	150	155
Gly	Val	Glu	Lys	Val	Lys	Ser	Pro	Ile	Ala	Glu	Met	Leu	Glu	Thr	Leu	165	170	175
Asn	Asp	Gln	Glu	Glu	Ser	Pro	Ile	Ala	Glu	Thr	Leu	Glu	Thr	Met	Asn	180	185	190
Asp	Gln	Glu	Glu	Ser	Pro	Ile	Ala	Glu	Thr	Met	Asn	Asp	Gln	Glu	Glu	195	200	205
Ser	Pro	Ile	Ala	Glu	Thr	Leu	Glu	Asn	Leu	Asn	Asp	Gln	Ala	Glu	Ser	210	215	220
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Ile	Ala	Glu	Met	Leu	Asp	Thr	Leu	Asn	Asp	Gln	Glu	Pro	Val	Ala	Val	245	250	255
Ala	Gln	Ser	Val	Val	Ser	Thr	Glu	Ser	Thr	Gln	Ala	Thr	Gly	Gln	Gln	260	265	270
Gln	Lys	Thr	Arg	Gly	Lys	Ser	Pro	Arg	Ser	Ser	Gly	Val	Lys	Asn	Val	275	280	285
Arg	Gln	Arg	Pro	Arg	Lys	Ala	Leu	Leu	Ser	Ser	Ser	Ser	Gly	Arg	Ser	290	295	300
Pro	Leu	Arg	Ile	Leu	Gln	Glu	Asp	Asn	Ser	Pro	Asn	Thr	Asn	Thr	Gln	305	310	315
His	Arg	Gln	Ala	Lys	Lys	Leu	Ser	Phe	Gln	Ser	Glu	Pro	Ala	Leu	Pro	325	330	335
His	Arg	Ala	Leu	Lys	Ile	Ser	His	Pro	Asn	Trp	Glu	Ser	Ser	Leu	Asn	340	345	350
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<210> 4

<211> 1426

<212> DNA

<213> Mus musculus

<400> 4

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caagcaagtg gctcgagtag cagaccctcg ttcacctagt gctggcatcc agcgcactcc	180
tattcaggtg gagagctctc cacagccaag cctaccagca gaacagctga acggtctcaa	240
acaggcacia gaccagatc cccgctctcc tactcttggc attgcacgga cacccatgaa	300
gatcagtggg ccagaccctc agtgctcact ggtgaaagag ctgagcgaag tattggagac	360
agaagcgtcg gaatcgattt cctccccaga gcttgctctg ccccgggaaa cgcctttatt	420
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gagccaggct gaactcgatc ccaaacaggt gtttaccaag gaggaagcca aacaatccgc	540
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gtcctcaggt tctaagcgca gcagacgaaa agcaaacagc aagggttctag ggaggtcccc	660
tctcaccatc ctgcaggatg acaactcccc tgggaccttg acactacgac agggtaagcg	720
gccttctgcc ctgagtgaga acgttaagga cctaaaggaa ggagtcgttc ttggaactgg	780
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<210> 5

<211> 1139

<212> DNA

<213> Homo sapiens

<400> 5

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agtcacacca gcgcggcctc cgccgcacaa caagcatctg gctcgagtgg cggacccccg      180
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cctaccagca ggggagcaac tggagggtct taaacatgcc caggactcag atccccgctc      300
tcctactctt ggtattgcac ggacacctat gaagaccagc agtggagacc cccaagccc      360
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cgacaagccc tcaagggacc ctgagactcc cagatcttca ggttctatgc gcaatagatg      660
gaaaccaaac agcagcaagg tactagggag atccccctc accatcctgc aggatgacaa      720
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<210> 6

<211> 822

<212> DNA

<213> Xenopus laevis

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<221> misc_feature

<222> (720)..(720)

<223> wherein n is g, a, t or c

<220>

<221> misc_feature

<222> (733)..(733)

<223> wherein n is g, a, t or c

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accctcgttc acctagtgtc ggcatccagc gcactcctat tcaggtagag agctctccac	180
agccaagcct accagcagaa cagctgaacg gtctcaaaca ggcacaagac ccagatcccc	240
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gctcactggg gaaagagctg agcgaagtat tggagacaga agcgtcggaa tcgatttcct	360
ccccagagct tgctctgccc cgggaaacgc ctttatttta tgacctggac ctgtcttcag	420
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gacgaaaagc aaacagcaag gttctagggg ggtccccctct cacatcctgc agatgacact	660
cccctgggac ttgacctacg acaggtagcg gcctctgcct catgagacgt taagactaan	720
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<210> 7

<211> 17

<212> PRT

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<213> Artificial Sequence

<220>

<223> synthetic peptide used as internal standard

<220>

<221> MOD_RES

<222> (8) .. (8)

<223> PHOSPHORYLATION

<220>

<221> MISC_FEATURE

<223> 13Cx6 labeled

<400> 7

Asn	Glu	Gly	Pro	Gln	Lys	Gly	Ser	Pro	Val	Ser	Ser	Trp	Arg	Thr	Asn
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Asn